

0590



7 1/17 1761

1761

RAW SEQUENCE LISTING

DATE: 02/05/2002

PATENT APPLICATION: US/09/909,464A

TIME: 12:16:21

Input Set : A:\PTO_VSK.txt

Output Set: N:\CRF3\02052002\I909464A.raw

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3 <110> APPLICANT: Lanahan, Michael
 4 Miller , Edward S.
 5 Kelly, Robert M.
 7 <120> TITLE OF INVENTION: METHODS FOR HIGH-TEMPERATURE HYDROLYSIS OF GALACTOSE-
 CONTAINING

8 OLIGOSACCHARIDES IN COMPLEX MIXTURES
 10 <130> FILE REFERENCE: 9207.4
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/909,464A
 C--> 12 <141> CURRENT FILING DATE: 2001-07-19
 12 <150> PRIOR APPLICATION NUMBER: US 60/220,211
 13 <151> PRIOR FILING DATE: 2000-07-22
 15 <160> NUMBER OF SEQ ID NOS: 2
 17 <170> SOFTWARE: PatentIn version 3.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1659
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Thermotoga maritima
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (1)..(1659)
 27 <223> OTHER INFORMATION:
 30 <400> SEQUENCE: 1

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FEB 13 2002

TC 1700

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33 1 5 10 15	
35 gag aaa aac ttc aca gtt gag ttc gcg gtg gag aag ata cac ctt ggc	
36 Glu Lys Asn Phe Thr Val Glu Phe Ala Val Glu Lys Ile His Leu Gly	
37 20 25 30	
39 tgg aag atc tcc ggc agg gtg aag gga agt ccg gga agg ctt gag gtt	
40 Trp Lys Ile Ser Gly Arg Val Lys Gly Ser Pro Gly Arg Leu Glu Val	
41 35 40 45	
43 ctt cga acg aaa gca ccg gaa aag gta ctt gtg aac aac tgg cag tcc	192
44 Leu Arg Thr Lys Ala Pro Glu Lys Val Leu Val Asn Asn Trp Gln Ser	
45 50 55 60	
47 tgg gga ccg tgc agg gtg gtc gat gcc ttt tct ttc aaa cca cct gaa	240
48 Trp Gly Pro Cys Arg Val Val Asp Ala Phe Ser Phe Lys Pro Pro Glu	
49 65 70 75 80	
51 ata gat ccg aac tgg aga tac acc gct tcg gtg gtg ccc gat gta ctt	288
52 Ile Asp Pro Asn Trp Arg Tyr Thr Ala Ser Val Val Pro Asp Val Leu	
53 85 90 95	
55 gaa agg aac ctc cag agc gac tat ttc gtg gct gaa gaa gga aaa gtg	336
56 Glu Arg Asn Leu Gln Ser Asp Tyr Phe Val Ala Glu Glu Gly Lys Val	
57 100 105 110	
59 tac ggt ttt ctg agt tcg aaa atc gca cat cct ttc ttc gct gtg gaa	384

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61			115					120					125				
63	gat	ggg	gaa	ctt	gtg	gca	tac	ctc	gaa	tat	ttc	gat	gtc	gag	ttc	gac	432
64	Asp	Gly	Glu	Leu	Val	Ala	Tyr	Leu	Glu	Tyr	Phe	Asp	Val	Glu	Phe	Asp	
65		130					135					140					
67	gac	ttt	gtt	cct	ctt	gaa	cct	ctc	gtt	gta	ctc	gag	gat	ccc	aac	aca	480
68	Asp	Phe	Val	Pro	Leu	Glu	Pro	Leu	Val	Val	Leu	Glu	Asp	Pro	Asn	Thr	
69	145					150					155					160	
71	ccc	ctt	ctt	ctg	gag	aaa	tac	gcg	gaa	ctc	gga	atg	gaa	aac	aac		528
72	Pro	Leu	Leu	Leu	Glu	Lys	Tyr	Ala	Glu	Leu	Val	Gly	Met	Glu	Asn	Asn	
73				165					170					175			
75	gcg	aga	gtt	cca	aaa	cac	aca	ccc	act	gga	tgg	tgc	agc	tgg	tac	cat	576
76	Ala	Arg	Val	Pro	Lys	His	Thr	Pro	Thr	Gly	Trp	Cys	Ser	Trp	Tyr	His	
77			180						185					190			
79	tac	ttc	ctt	gat	ctc	acc	tgg	gaa	gag	acc	ctc	aag	aac	ctg	aag	ctc	624
80	Tyr	Phe	Leu	Asp	Leu	Thr	Trp	Glu	Glu	Thr	Leu	Lys	Asn	Leu	Lys	Leu	
81			195					200					205				
83	gcg	aag	aat	ttc	ccg	ttc	gag	gtc	ttc	cag	ata	gac	gac	gcc	tac	gaa	672
84	Ala	Lys	Asn	Phe	Pro	Phe	Glu	Val	Phe	Gln	Ile	Asp	Asp	Ala	Tyr	Glu	
85		210				215					220						
87	aag	gac	ata	ggt	gac	tgg	ctc	gtg	aca	aga	gga	gac	ttt	cca	tcg	gtg	720
88	Lys	Asp	Ile	Gly	Asp	Trp	Leu	Val	Thr	Arg	Gly	Asp	Phe	Pro	Ser	Val	
89	225			230						235					240		
91	gaa	gag	atg	gca	aaa	ggt	ata	gcg	gaa	aac	ggt	ttc	atc	ccg	ggc	ata	768
92	Glu	Glu	Met	Ala	Lys	Val	Ile	Ala	Glu	Asn	Gly	Phe	Ile	Pro	Gly	Ile	
93				245					250					255			
95	tgg	acc	gcc	ccg	ttc	agt	gtt	tct	gaa	acc	tcg	gat	gta	ttc	aac	gaa	816
96	Trp	Thr	Ala	Pro	Phe	Ser	Val	Ser	Glu	Thr	Ser	Asp	Val	Phe	Asn	Glu	
97			260					265					270				
99	cat	ccg	gac	tgg	gta	gtg	aag	gaa	aac	gga	gag	ccg	aag	atg	gct	tac	864
100	His	Pro	Asp	Trp	Val	Val	Lys	Glu	Asn	Gly	Glu	Pro	Lys	Met	Ala	Tyr	
101			275					280					285				
103	aga	aac	tgg	aac	aaa	aag	ata	tac	gcc	ctc	gat	ctt	tcg	aaa	gat	gag	912
104	Arg	Asn	Trp	Asn	Lys	Lys	Ile	Tyr	Ala	Leu	Asp	Leu	Ser	Lys	Asp	Glu	
105		290				295					300						
107	gtt	ctg	aac	tgg	ctt	ttc	gat	ctc	ttc	tca	tct	ctg	aga	aag	atg	ggc	960
108	Val	Leu	Asn	Trp	Leu	Phe	Asp	Leu	Phe	Ser	Ser	Leu	Arg	Lys	Met	Gly	
109	305			310						315					320		
111	tac	agg	tac	ttc	aag	atc	gac	ttt	ctc	ttc	gcg	ggt	gcc	gtt	cca	gga	1008
112	Tyr	Arg	Tyr	Phe	Lys	Ile	Asp	Phe	Leu	Phe	Ala	Gly	Ala	Val	Pro	Gly	
113				325					330					335			
115	gaa	aga	aaa	aag	aac	ata	aca	cca	att	cag	gcg	ttc	aga	aaa	ggg	att	1056
116	Glu	Arg	Lys	Lys	Asn	Ile	Thr	Pro	Ile	Gln	Ala	Phe	Arg	Lys	Gly	Ile	
117			340					345						350			
119	gag	acg	atc	aga	aaa	gcg	gtg	gga	gaa	gat	tct	ttc	atc	ctc	gga	tgc	1104
120	Glu	Thr	Ile	Arg	Lys	Ala	Val	Gly	Glu	Asp	Ser	Phe	Ile	Leu	Gly	Cys	
121			355					360					365				
123	ggc	tct	ccc	ctt	ctt	ccc	gca	gtg	gga	tgc	gtc	gac	ggg	atg	agg	ata	1152
124	Gly	Ser	Pro	Leu	Leu	Pro	Ala	Val	Gly	Cys	Val	Asp	Gly	Met	Arg	Ile	

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127 gga cct gac act gcg ccg ttc tgg gga gaa cat ata gaa gac aac gga      1200
128 Gly Pro Asp Thr Ala Pro Phe Trp Gly Glu His Ile Glu Asp Asn Gly
129 385      390      395      400
131 gct ccc gct gca aga tgg gcg ctg aga aac gcc ata acg agg tac ttc      1248
132 Ala Pro Ala Ala Arg Trp Ala Leu Arg Asn Ala Ile Thr Arg Tyr Phe
133      405      410      415
135 atg cac gac agg ttc tgg ctg aac gac ccc gac tgt ctg ata ctg aga      1296
136 Met His Asp Arg Phe Trp Leu Asn Asp Pro Asp Cys Leu Ile Leu Arg
137      420      425      430
139 gag gag aaa acg gat ctc aca cag aag gaa aag gag ctc tac tcg tac      1344
140 Glu Glu Lys Thr Asp Leu Thr Gln Lys Glu Lys Glu Leu Tyr Ser Tyr
141      435      440      445
143 acg tgt gga gtg ctc gac aac atg atc ata gaa agc gat gat ctc tcg      1392
144 Thr Cys Gly Val Leu Asp Asn Met Ile Ile Glu Ser Asp Asp Leu Ser
145      450      455      460
147 ctc gtc aga gat cat gga aaa aag gtt ctg aaa gaa acg ctc gaa ctc      1440
148 Leu Val Arg Asp His Gly Lys Lys Val Leu Lys Glu Thr Leu Glu Leu
149 465      470      475      480
151 ctc ggt gga aga cca cgg gtt caa aac atc atg tcg gag gat ctg aga      1488
152 Leu Gly Gly Arg Pro Arg Val Gln Asn Ile Met Ser Glu Asp Leu Arg
153      485      490      495
155 tac gag atc gtc tcg tct ggc act ctc tca gga aac gtc aag atc gtg      1536
156 Tyr Glu Ile Val Ser Ser Gly Thr Leu Ser Gly Asn Val Lys Ile Val
157      500      505      510
159 gtc gat ctg aac agc aga gag tac cac ctg gaa aaa gaa gga aag tcc      1584
160 Val Asp Leu Asn Ser Arg Glu Tyr His Leu Glu Lys Glu Gly Lys Ser
161      515      520      525
163 tcc ctg aaa aaa aga gtc gtc aaa aga gaa gac gga aga aac ttc tac      1632
164 Ser Leu Lys Lys Arg Val Val Lys Arg Glu Asp Gly Arg Asn Phe Tyr
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167 ttc tac gaa gag ggt gag aga gaa tga      1659
168 Phe Tyr Glu Glu Gly Glu Arg Glu
169 545      550
172 <210> SEQ ID NO: 2
173 <211> LENGTH: 552
174 <212> TYPE: PRT
175 <213> ORGANISM: Thermotoga maritima
177 <400> SEQUENCE: 2
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184      20      25      30
187 Trp Lys Ile Ser Gly Arg Val Lys Gly Ser Pro Gly Arg Leu Glu Val
188      35      40      45
191 Leu Arg Thr Lys Ala Pro Glu Lys Val Leu Val Asn Asn Trp Gln Ser
192      50      55      60
195 Trp Gly Pro Cys Arg Val Val Asp Ala Phe Ser Phe Lys Pro Pro Glu
196 65      70      75      80

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199 Ile Asp Pro Asn Trp Arg Tyr Thr Ala Ser Val Val Pro Asp Val Leu
200      85      90      95
203 Glu Arg Asn Leu Gln Ser Asp Tyr Phe Val Ala Glu Glu Gly Lys Val
204      100      105      110
207 Tyr Gly Phe Leu Ser Ser Lys Ile Ala His Pro Phe Phe Ala Val Glu
208      115      120      125
211 Asp Gly Glu Leu Val Ala Tyr Leu Glu Tyr Phe Asp Val Glu Phe Asp
212      130      135      140
215 Asp Phe Val Pro Leu Glu Pro Leu Val Val Leu Glu Asp Pro Asn Thr
216 145      150      155      160
219 Pro Leu Leu Leu Glu Lys Tyr Ala Glu Leu Val Gly Met Glu Asn Asn
220      165      170      175
223 Ala Arg Val Pro Lys His Thr Pro Thr Gly Trp Cys Ser Trp Tyr His
224      180      185      190
227 Tyr Phe Leu Asp Leu Thr Trp Glu Glu Thr Leu Lys Asn Leu Lys Leu
228      195      200      205
231 Ala Lys Asn Phe Pro Phe Glu Val Phe Gln Ile Asp Asp Ala Tyr Glu
232      210      215      220
235 Lys Asp Ile Gly Asp Trp Leu Val Thr Arg Gly Asp Phe Pro Ser Val
236 225      230      235      240
239 Glu Glu Met Ala Lys Val Ile Ala Glu Asn Gly Phe Ile Pro Gly Ile
240      245      250      255
243 Trp Thr Ala Pro Phe Ser Val Ser Glu Thr Ser Asp Val Phe Asn Glu
244      260      265      270
247 His Pro Asp Trp Val Val Lys Glu Asn Gly Glu Pro Lys Met Ala Tyr
248      275      280      285
251 Arg Asn Trp Asn Lys Lys Ile Tyr Ala Leu Asp Leu Ser Lys Asp Glu
252      290      295      300
255 Val Leu Asn Trp Leu Phe Asp Leu Phe Ser Ser Leu Arg Lys Met Gly
256 305      310      315      320
259 Tyr Arg Tyr Phe Lys Ile Asp Phe Leu Phe Ala Gly Ala Val Pro Gly
260      325      330      335
263 Glu Arg Lys Lys Asn Ile Thr Pro Ile Gln Ala Phe Arg Lys Gly Ile
264      340      345      350
267 Glu Thr Ile Arg Lys Ala Val Gly Glu Asp Ser Phe Ile Leu Gly Cys
268      355      360      365
271 Gly Ser Pro Leu Leu Pro Ala Val Gly Cys Val Asp Gly Met Arg Ile
272      370      375      380
275 Gly Pro Asp Thr Ala Pro Phe Trp Gly Glu His Ile Glu Asp Asn Gly
276 385      390      395      400
279 Ala Pro Ala Ala Arg Trp Ala Leu Arg Asn Ala Ile Thr Arg Tyr Phe
280      405      410      415
283 Met His Asp Arg Phe Trp Leu Asn Asp Pro Asp Cys Leu Ile Leu Arg
284      420      425      430
287 Glu Glu Lys Thr Asp Leu Thr Gln Lys Glu Lys Glu Leu Tyr Ser Tyr
288      435      440      445
291 Thr Cys Gly Val Leu Asp Asn Met Ile Ile Glu Ser Asp Asp Leu Ser
292      450      455      460
295 Leu Val Arg Asp His Gly Lys Lys Val Leu Lys Glu Thr Leu Glu Leu

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296 465                               470                               475                               480
299 Leu Gly Gly Arg Pro Arg Val Gln Asn Ile Met Ser Glu Asp Leu Arg
300                               485                               490                               495
303 Tyr Glu Ile Val Ser Ser Gly Thr Leu Ser Gly Asn Val Lys Ile Val
304                               500                               505                               510
307 Val Asp Leu Asn Ser Arg Glu Tyr His Leu Glu Lys Glu Gly Lys Ser
308                               515                               520                               525
311 Ser Leu Lys Lys Arg Val Val Lys Arg Glu Asp Gly Arg Asn Phe Tyr
312                               530                               535                               540
315 Phe Tyr Glu Glu Gly Glu Arg Glu
316 545                               550

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VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date